



SEQUENCE LISTING

<110> Fitzgerald, David J.
Mrsny, Randall J.
The Government of the United States of America
as represented by The Secretary of the
Department of Health and Human Services
Genentech, Inc.

<120> Pseudomonas Exotoxin A-Like Chimeric Immunogens for
Eliciting a Secretory IgA-Mediated Immune Response

<130> 015280-361200US

<140> US 10/659,036

<141> 2003-09-09

<150> US 60/056,924

<151> 1997-07-11

<150> WO PCT/US98/14336

<151> 1998-07-10

<150> US 09/462,713

<151> 2000-05-12

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1839

<212> DNA

<213> Pseudomonas aeruginosa

<220>

<221> CDS

<222> (1)..(1839)

<223> exotoxin A

<400> 1

gcc gaa gaa gct ttc gac ctc tgg aac gaa tgc gcc aaa gcc tgc gtg	48
Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val	
1 5 10 15	

ctc gac ctc aag gac ggc gtg cgt tcc agc cgc atg agc gtc gac ccg	96
Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro	
20 25 30	

gcc atc gcc gac acc aac ggc cag ggc gtg ctg cac tac tcc atg gtc	144
Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val	
35 40 45	

ctg gag ggc ggc aac gac gcg ctc aag ctg gcc atc gac aac gcc ctc	192
Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu	
50 55 60	

agc atc acc agc gac ggc ctg acc atc cgc ctc gaa ggc ggc gtc gag	240
Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu	
65 70 75 80	

ccg aac aag ccg gtg cgc tac agc tac acg cgc cag gcg cgc ggc agt	288
Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser	
85 90 95	
tgg tcg ctg aac tgg ctg gta ccg atc ggc cac gag aag ccc tcg aac	336
Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn	
100 105 110	
atc aag gtg ttc atc cac gaa ctg aac gcc ggc aac cag ctc agc cac	384
Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His	
115 120 125	
atg tcg ccg atc tac acc atc gag atg ggc gac gag ttg ctg gcg aag	432
Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys	
130 135 140	
ctg gcg cgc gat gcc acc ttc ttc gtc agg gcg cac gag agc aac gag	480
Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu	
145 150 155 160	
atg cag ccg acg ctc gcc atc agc cat gcc ggg gtc agc gtg gtc atg	528
Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met	
165 170 175	
gcc cag acc cag ccg cgc cgg gaa aag cgc tgg agc gaa tgg gcc agc	576
Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser	
180 185 190	
ggc aag gtg ttg tgc ctg ctc gac ccg ctg gac ggg gtc tac aac tac	624
Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr	
195 200 205	
ctc gcc cag caa cgc tgc aac ctc gac gat acc tgg gaa ggc aag atc	672
Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile	
210 215 220	
tac cgg gtg ctc gcc ggc aac ccg gcg aag cat gac ctg gac atc aaa	720
Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys	
225 230 235 240	
ccc acg gtc atc agt cat cgc ctg cac ttt ccc gag ggc ggc agc ctg	768
Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu	
245 250 255	
gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag act ttc	816
Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe	
260 265 270	
acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag tgc ggc	864
Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly	
275 280 285	
tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg cgg ctg tcg	912
Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser	
290 295 300	
tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc ccc ggc	960
Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly	
305 310 315 320	

agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag cag gcc	1008
Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala	
325 330 335	
cgT ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc gtc cgg	1056
Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg	
340 345 350	
cag ggc acc ggc aac gac gag gcc gcc gcg gcc aac gcc gac gtg gtg	1104
Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val	
355 360 365	
agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg gcc ccg gcg gac	1152
Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp	
370 375 380	
agc ggc gac gcc ctg ctg gag cgc aac tat ccc act gcc gcg gag ttc	1200
Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe	
385 390 395 400	
ctc gcc gac gcc gcc gac gtc agc ttc agc acc cgc gcc acg cag aac	1248
Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn	
405 410 415	
tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag gag cgc	1296
Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg	
420 425 430	
ggc tat gtg ttc gtc gcc tac cac gcc acc ttc ctc gaa gcg gcg caa	1344
Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln	
435 440 445	
agc atc gtc ttc gcc ggg gtg cgc gcg cgc agc cag gac ctc gac gcg	1392
Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala	
450 455 460	
atc tgg cgc ggt ttc tat atc gcc gcc gat ccg gcg ctg gcc tac gcc	1440
Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly	
465 470 475 480	
tac gcc cag gac cag gaa ccc gac gca cgc gcc cgg atc cgc aac ggt	1488
Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly	
485 490 495	
gcc ctg ctg cgg gtc tat gtg ccg cgc tcg agc ctg ccg gcc ttc tac	1536
Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr	
500 505 510	
cgC acc agc ctg acc ctg gcc gcg ccg gag gcg gcg gcc gag gtc gaa	1584
Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu	
515 520 525	
cgG ctg atc gcc cat ccg ctg ccg ctg cgc ctg gac gcc atc acc gcc	1632
Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly	
530 535 540	
ccc gag gag gaa gcc ggg cgc ctg gag acc att ctc gcc tgg ccg ctg	1680
Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu	
545 550 555 560	

gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac cgc cgc 1728
Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
565 570 575

aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag gaa cag 1776
Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
580 585 590

gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa ccg ccg 1824
Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
595 600 605

cgc gag gac ctg aag 1839
 Arg Glu Asp Leu Lys
 610

 $\langle 210 \rangle$ 2

<211> 613

<212> PRT

<213> *Pseudomonas aeruginosa*

<220>

<223> exotoxin A

<400> 2

Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
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Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
165 170 175

Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
180 185 190

Gly	Lys	Val	Leu	Cys	Leu	Leu	Asp	Pro	Leu	Asp	Gly	Val	Tyr	Asn	Tyr	195	200	205	
Leu	Ala	Gln	Gln	Arg	Cys	Asn	Leu	Asp	Asp	Thr	Trp	Glu	Gly	Lys	Ile	210	215	220	
Tyr	Arg	Val	Leu	Ala	Gly	Asn	Pro	Ala	Lys	His	Asp	Leu	Asp	Ile	Lys	225	230	235	240
Pro	Thr	Val	Ile	Ser	His	Arg	Leu	His	Phe	Pro	Glu	Gly	Gly	Ser	Leu	245	250	255	
Ala	Ala	Leu	Thr	Ala	His	Gln	Ala	Cys	His	Leu	Pro	Leu	Glu	Thr	Phe	260	265	270	
Thr	Arg	His	Arg	Gln	Pro	Arg	Gly	Trp	Glu	Gln	Leu	Glu	Gln	Cys	Gly	275	280	285	
Tyr	Pro	Val	Gln	Arg	Leu	Val	Ala	Leu	Tyr	Leu	Ala	Ala	Arg	Leu	Ser	290	295	300	
Trp	Asn	Gln	Val	Asp	Gln	Val	Ile	Arg	Asn	Ala	Leu	Ala	Ser	Pro	Gly	305	310	315	320
Ser	Gly	Gly	Asp	Leu	Gly	Glu	Ala	Ile	Arg	Glu	Gln	Pro	Glu	Gln	Ala	325	330	335	
Arg	Leu	Ala	Leu	Thr	Leu	Ala	Ala	Ala	Glu	Ser	Glu	Arg	Phe	Val	Arg	340	345	350	
Gln	Gly	Thr	Gly	Asn	Asp	Glu	Ala	Gly	Ala	Ala	Asn	Ala	Asp	Val	Val	355	360	365	
Ser	Leu	Thr	Cys	Pro	Val	Ala	Ala	Gly	Glu	Cys	Ala	Gly	Pro	Ala	Asp	370	375	380	
Ser	Gly	Asp	Ala	Leu	Leu	Glu	Arg	Asn	Tyr	Pro	Thr	Gly	Ala	Glu	Phe	385	390	395	400
Leu	Gly	Asp	Gly	Gly	Asp	Val	Ser	Phe	Ser	Thr	Arg	Gly	Thr	Gln	Asn	405	410	415	
Trp	Thr	Val	Glu	Arg	Leu	Leu	Gln	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	420	425	430	
Gly	Tyr	Val	Phe	Val	Gly	Tyr	His	Gly	Thr	Phe	Leu	Glu	Ala	Ala	Gln	435	440	445	
Ser	Ile	Val	Phe	Gly	Gly	Val	Arg	Ala	Arg	Ser	Gln	Asp	Leu	Asp	Ala	450	455	460	
Ile	Trp	Arg	Gly	Phe	Tyr	Ile	Ala	Gly	Asp	Pro	Ala	Leu	Ala	Tyr	Gly	465	470	475	480
Tyr	Ala	Gln	Asp	Gln	Glu	Pro	Asp	Ala	Arg	Gly	Arg	Ile	Arg	Asn	Gly	485	490	495	
Ala	Leu	Leu	Arg	Val	Tyr	Val	Pro	Arg	Ser	Ser	Leu	Pro	Gly	Phe	Tyr	500	505	510	

[illegible]

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<210> 3
<211> 35
<212> PRT
<213> Human immunodeficiency virus type 1
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<220>
<221> PEPTIDE
<222> (1)..(35)
<223> V3 loop of MN strain of HIV-1
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<400> 3
Cys Thr Arg Pro Asn Tyr Asn Lys Arg Lys Arg Ile His Ile Gly Pro
1 5 10 15

Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr Ile Arg Gln
20 25 30

Ala His Cys
35

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<210> 4
<211> 35
<212> PRT
<213> Human immunodeficiency virus type 1
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<220>
<221> PEPTIDE
<222> (1)..(35)
<223> V3 loop of Thai-E strain of HIV-1
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<400> 4
Cys Thr Arg Pro Ser Asn Asn Thr Arg Thr Ser Ile Thr Ile Gly Pro
1 5 10 15

Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp Ile Arg Lys
 20 25 30

Ala Tyr Cys
 35

<210> 5
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: coding strand
 of duplex containing novel PstI site

<400> 5
 tggccctgac cctggccgcc gccgagagcg agcgcttcgt ccggcagggc accggcaacg 60
 acgaggccgg cgcggaacac ctgcagggcc 90

<210> 6
 <211> 24
 <212> PRT
 <213> Pseudomonas aeruginosa

<220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Ib loop region of wild-type Pseudomonas exotoxin A

<400> 6
 Gly Ala Ala Asn Ala Asp Val Val Ser Leu Thr Cys Pro Val Ala Ala
 1 5 10 15

Gly Glu Cys Ala Gly Pro Ala Asp
 20

<210> 7
 <211> 28
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ib loop region
 of ntPE-V3MN14

<400> 7
 Gly Ala Ala Asn Leu His Cys Gly Ile His Ile Gly Pro Gly Arg Ala
 1 5 10 15

Phe Tyr Thr Thr Lys Cys Met Gln Gly Pro Ala Asp
 20 25

<210> 8
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region
of ntPE-V3MN26

<400> 8

Gly Ala Ala Asn Leu His Cys Asn Tyr Asn Lys Arg Lys Arg Ile His
1 5 10 15

Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Lys Asn Ile Ile Gly Thr
20 25 30

Ile Cys Met Gln Gly Pro Ala Asp
35 40

<210> 9

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region
of ntPE-V3Th-E26

<400> 9

Gly Ala Ala Asn Leu His Cys Ser Asn Asn Thr Arg Thr Ser Ile Thr
1 5 10 15

Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly Asp Ile Ile Gly Asp
20 25 30

Asp Ile Cys Met Gln Gly Pro Ala Asp
35 40

<210> 10

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ib loop region
of ntPE-fp16

<400> 10

Gly Ala Ala Asn Leu Gln Cys Arg Leu Glu Glu Lys Lys Gly Asn Tyr
1 5 10 15

Val Val Thr Asp His Arg Leu Cys Leu Gln Gly Pro Ala Asp
20 25 30

<210> 11

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:endoplasmic
reticulum (ER) retention sequence

<400> 11
Arg Glu Asp Leu Lys
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<210> 12
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 12
Arg Glu Asp Leu
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<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: endoplasmic
reticulum (ER) retention sequence

<400> 13
Lys Asp Glu Leu
1